

100260" 62828860



#2

1 / 16

1 GCTGTGGGAA CCTCTCCAG CGCACGAACT CAGCCAAACGA TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCAGC
CGACACCCCTT GGAGAGGTGC GCGTGTCTGA GTCGGTTGCT AAAGACTATC TAAAAACCTT CAAACTGGTC TCTACGTCC CCACTTCCCTC CGGAAGGATG

101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCC GGCCTGCTGA TGGCCGAGGC AGGGTCCGAC CCAGGACCCA GGACGGCGTC GGAACACATA CCATGGCCCG
GCAATCCCTT GAGACCCCTG TCTCGCGGG TCTCGCGGG CCGCGGACT ACCGGCTCC TCCACGCTG GGTCTGGGT CCTTGGTAT GGTACCGGGC
MetalArg

201 GATCCCAAG ACCTAAAGT TCGTGTGCTG CATCGTCGG GTCTGTCTGC CAGTCTAGC TTAATCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
CTAGGGGTC TGGGATTTCA AGCAGCAGCA GTAGCAGCG CAGGACGACG GTACGATCG AATGAGACGG TGGTACGGG CCGTCTCTCT TCAAGGGGTC

4 IleProLys ThrLeuLys heValValva lileValala ValLeuLeup roValleuAl aTyrSerAla ThrThrAlaA rgGlnGluG l uValProGln

301 CAGACAGTGG CCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
GTCTGTCCAC GGGGTGCTGT TGTCTCCGTG TCGAAGTTCC CCCTCCTCAC AGGTCTCTCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT

37 GlnThrVala laProGlnG l nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCyS AsnProCysThr

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAA CATAAAAGTT CCTGCACCAT
GTCTCCACA CCTAATGTGG TTGCGAAGGT TGTACTTGG AAGAACGAAG GGTACATGTC AACATTTAG TCTAGTTTT GTATTTTCAA GGACGTGGTA

71 GluGlyVa lasPtyrThr AsnAlaSera snAnGluPr oSerCysPhe ProCysThrV alcCysLysSe raspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGT
CTGGTCTCTG TGTACACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTACACATCGT CCACGGGATC ACCCTTTG

104 ThrArgasp ThrValCySg l nCysLysG l uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSera rgCysProse rGlyGlu

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAAT GCCACTGTGG AAACCCACG TCGTGAAGAG ACAATGAAC
GTTTCAGTCAT TAACATGCAG GACCCCTACTA TAGGTACACAC AACTTCTTAA ACCACGGTTA CCGTGACACC TTTGGGGTGC AGCACTTCTC TGTACTTGT

137 GlnValSera snCysThrSe rTrpAspAsp lileGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aalaGluGlu ThrMetAsnThr

701 CCAGCCCGGG GACTCCTGCC CCAGCTGCTG AACAGACAAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG
GGTCGGGGCC CTGAGGACGG GGTGACGAC TTTCTCTGTTA CTGTGTGCTG GGTCCCTGAG GACGGGGTGC ACCACTTCTC TGTACTGTT GGTGCGGGCC

171 SerProGl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrp roAlaProAl aalaGluGlu ThrMetThrT hrSerProGly

FIG. 1A-1

801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG GACTCCTGCC
 CTGAGGACGG GGTGACGAC GGTGACGAC TCTCTGTGTA CTGGTGGTGG GGGCCCTGAG GACGGGGTGG ACGACTTCTC TGTTACTGGT GGTGGGGCCC CTGAGGACGG
 204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla
 901 TCTTCTCATTT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTT GAAAGACTTC ACTGTGGAAG AAATTCCCTTC
 AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCTAGTATC AAGATTAAAC CAAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG
 237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIleVal lLeuIleVal lLeuIleVal ValPheVal
 1001 CTTACCTGAA AGGTTACAGT AGGGCTGGC TGAGGGGGGG GGGGGCTGGA CACTCTCTGC CCTGCCCTCCC TCTGCTGTGT TCCCACAGAC AGAAACGCCCT
 GAATGGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCGCGGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGTGTCTG TCTTTGCGGA
 1101 GCCCTGCC CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA CAAAAA
 CCGGGACGG GTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG. 1A-2

1 GCTGTGGGAA CCTCTCCAG CGACGAACT CAGCCAAACA TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
 CGACACCCCTT GGAGAGGTGC GCGTGCTGA GTCGGTTGCT AAAGACTATC TAAAAACCCCT CAAACTGGTC TCTAGCTTCC CCCTTCCTC GCGAAGGATG
 MetGlnG l yValLysGlu ArgPheLeuPro
 -40
 101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GCGCGCTGA TGGCCGAGGC AGGTGCGAC CCAGGACCCA GGACGGCGTC GGAACCCATA CCATGGCCCCG
 GCAATCCCTT GAGACCCCTG TCTCGGGGG TCTCGGGGG CCGGGGACT ACCGGCTCG TCCCACGCTG GGTCTGGGT CCTTGGTAT GGTACCGGGC
 -30 LeuGlyAs nSerGlyAsp ArgAlaProA rgProProAs pGlyArgGly ArgValArgP roArgThrGl nAspGlyVal GlyAsnHisT hrMetAlaArg
 201 GATCCCCAAG ACCCTAAAGT TCGTGTGCTG CATCGTCGG GTCTGTGCTG CAGTCTTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
 CTAGGGGTTC TGGGATTCA AGCAGCAGCA GTAGCAGCG CAGGACGACG GTGAGGATCG AATGAGACGG TGGTACGGG CCGTCTCTCT TCAAGGGGTC
 4 IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluG l uValProGln
 301 CAGACAGTGG CCCACAGCA ACAGAGGGCAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
 GTCTGTACCC GGGGTGCTG TGTCTCCGT TCGAAGTTCC CCTCTCTCAC AGCTGCTCT AGAGTATCTA GTCTTGTATG ACCTGGACA TTGGGCACGT
 37 GlnThrVala laProGlnG l nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCy s AsnProCy sThr

FIG. 1B-1

401 CAGAGGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT
GTCTCCACCA CCTAATGTGG TTGCGAAGGT TGTACTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA

71 GluglyVa LasptyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alcysLyase rAspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGCACCCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC
CTGGTCTCTG TGTACACACAG TCACATTCTT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCTTTCAG

104 ThrArgasp ThrValcysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG
ThrArgasp ThrValcysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAAAT TGGTGCCAAT GCCACTGTGG AAACCCCCAGC TGCTGAAGAG ACAATGAACA
GTTCAAGTCAT TAACATGCAG GACCCCTACTA TAGGTACACAC AACTTCTTAA ACCACGGTTA CCGGTGACACC TTTGGGGTGG ACGACTTCTC TGTACTTGT

137 GlnValSerA sncysThrSe rTrpAspAsp lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG
GlnValSerA sncysThrSe rTrpAspAsp lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG lncysLysG

701 CCAGCCCCGG GACTCCTGCC CCAGCTGCTG AAGACACAAT GAACACCAGC CCAGGGACTC CTGCCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG
GGTGGGGGCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGCTGTC GGTCCCTGAG GACGGGGTGG ACGACTTCTC TGTACTTGT GGTGGGGGCC

171 SerProgl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly

801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACACACAGC CCGGGGACTC CTGCCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG GACTCCTGCC
CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGCTGTC GGTCCCTGAG GACGGGGTGG ACGACTTCTC TGTACTTGT GGTGGGGGCC CTGAGGACGG

204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly yThrProAla

901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTC GAAAGACTTC ACTGTGGAAG AAATTCCTTC
AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCTACTATC AAGATTACCA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTAAAGGAAG

237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal
SerSerHist yrLeuSerCy sThrIleVal GlyIleIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal lLeuIleVal

1001 CTTACCTGAA AGGTTACAGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCCTCC TCTGCTGTGT TCCACACAGAC AGAAACGCCT
GAATGGACTT TCCAAGTCCA TCCGGGACCG ACTCCCGCCC CCGCGGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGTGTCTG TCTTTGCGGA

1101 GCCCTGCC CAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA
GGGAGACGG GTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG.-1B-2

Apo2 1 -----MEQRGQNAFAASGARKRHGPGPREARGARPGRLRVPKTI[↓]VL
 Apo2DcR 1 -----MARIPKTLKFVV
 DR4 51 GRGALPTSMGQHGPSARA[↓]RAGRAPH[↓]RPAREASPLRLRVHKTFFKFVVVGVL

Apo2 41 VVA[↓]AVLLLVSAESALIT[↓]OODLAPQORAAPOOKRSSPSEGLCPPGHHISED
 Apo2DcR 13 VIVAVLLPVLAYSA[↓]TATTARQEEVPQOTVAPOOQRHSFKGEECPAGSHRSEH
 DR4 101 LQVVPSSAATIK-----LHD[↑]SIGTQOWEHSPLGELCPPGSHRSEH

Apo2 91 GRDCISCKYGDY[↑]STHWN[↑]DLFLC[↑]LRCT[↑]RCD[↑]SGEVELSPCTTTRNTVCQCE
 Apo2DcR 63 TGACNECTEGVDYTNASNNEPSCFPC[↑]TVCKSDQKHKSSCTMTRD[↑]IVCQCK
 DR4 142 PGACNRCTEGVGYTNASN[↑]NLFA[↑]CLPCTACKSDE[↑]ERSPCTTTRNTACQCK

Apo2 141 EGTFREED[↑]SPEMCRKCR[↑]TGCP[↑]RGMVK[↑]VGDCTPWS[↑]DI[↑]ECVHKE-----
 Apo2DcR 113 EGTFRNENSPEMCRKCSR-CP[↑]SGEVQVSNCTSWDDI[↑]QCV[↑]E-EFGANATVE
 DR4 192 EGTFRNDNSAEMCRKCRSTGCP[↑]RGMVK[↑]VKDCTPWS[↑]DI[↑]ECVHKE-----

Apo2 -----
 Apo2DcR 161 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
 DR4 -----

Apo2 183 -----SGIIIGVTVA[↑]AVVLI[↑]VA[↑]FEV---
 Apo2DcR 211 ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
 DR4 234 -----SGNGHNIWVILV[↑]VTLV[↑]VPILL[↑]VAV-LIVC

Apo2 203 CKSLLWKKVL[↑]PYLK[↑]GICSGGGDP[↑]ERVDRSSQ[↑]RPGA[↑]EDNVLNEIVSILQP
 DR4 262 CCIGSGCGGDPKCM[↑]DRVCFWRLG[↑]LLRGPGAEDNAHNEILSNADSLSTFVS

Apo2 253 TQVPEOE[↑]MEV[↑]QEP[↑]AEPTG[↑]VNMLSPGESEHLL[↑]EP[↑]AEAE[↑]SQRRRL[↑]LPANE
 DR4 312 ----EQOMESQEPADLTGVT[↑]VQSPGEAQCLL[↑]GPAEAE[↑]GSQRRRL[↑]VPANG

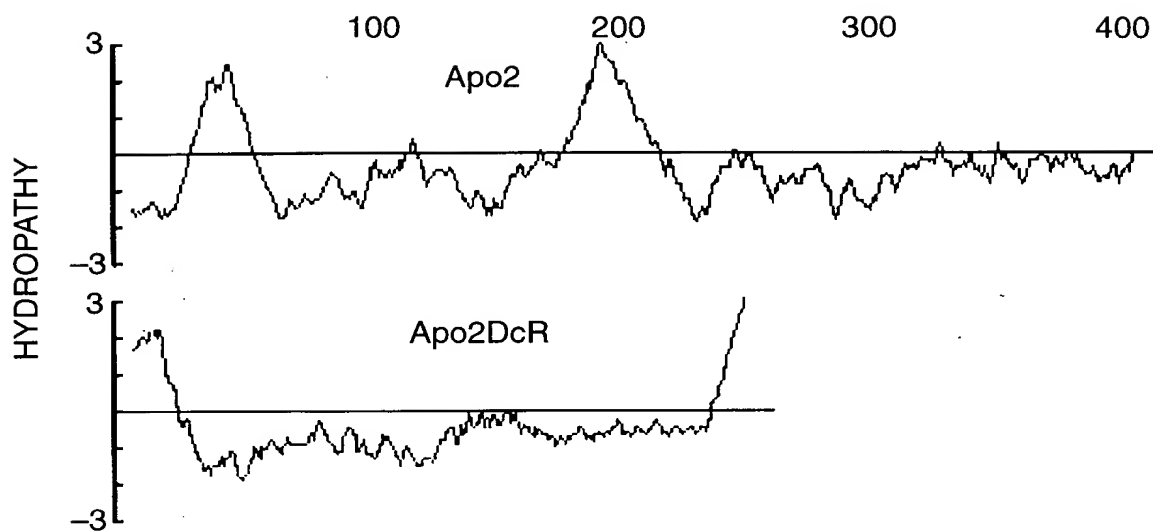
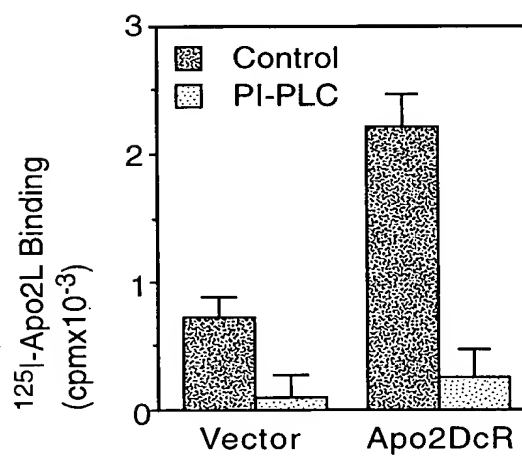
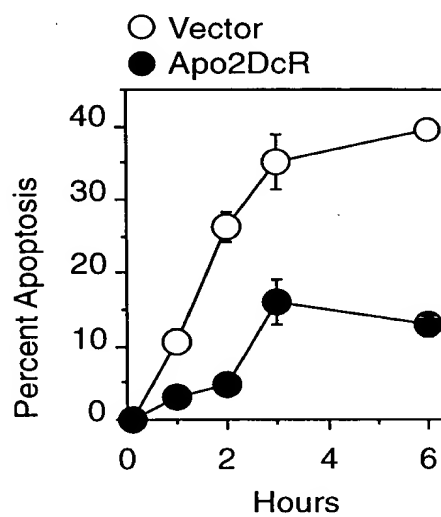
Apo2 303 GDPTETLRQCFDDFADLV[↑]PFDSWE[↑]FLMRK[↑]LGLMDNEIK[↑]VAKAEAAGH--R
 DR4 358 ADPTETILMLFFDKFANIV[↑]PFDSWDQ[↑]LMRQ[↑]LDLTKNEIDVVRAGTAGP--G
 Apo3/DR3 338 VMDAVPARRWKEFVRILGL[↑]REAEIEAVEVEI-GRF-R
 TNFR1 322 VVENVPPLRWKEFVRRGL[↑]SDHEIDRIELQ-GRCLR
 CD95 220 IAGVHTLSQVKG[↑]FVRKNGVNEAKIDEIKNDN-VQDTA

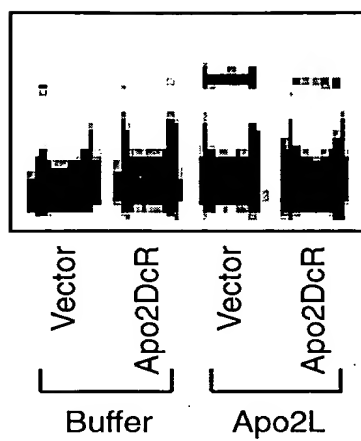
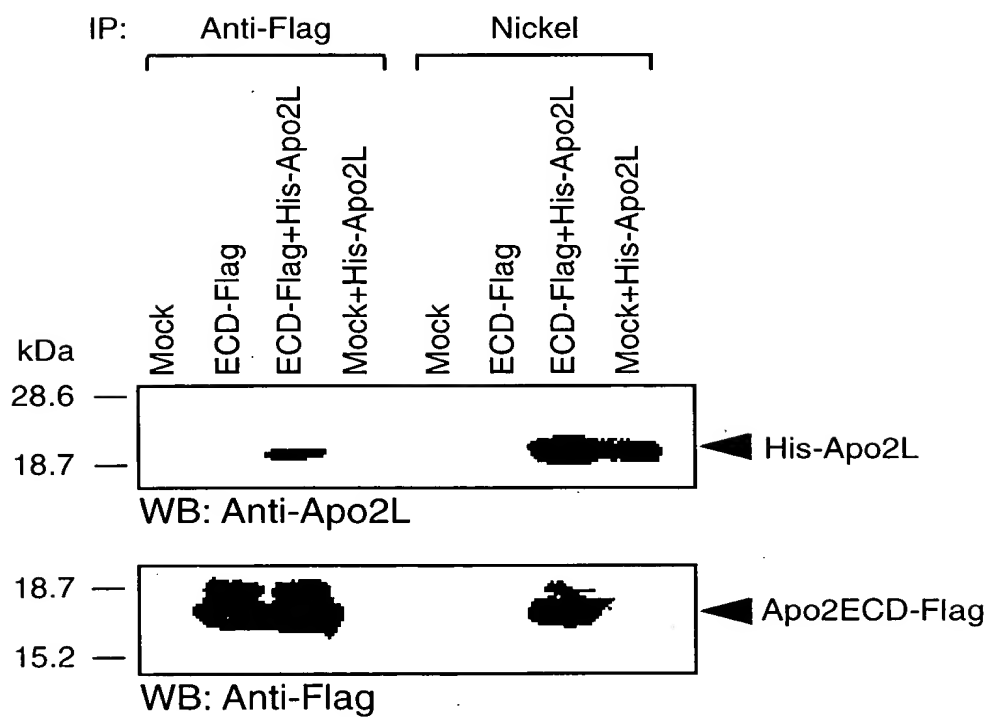
Apo2 351 DTLYTMLIKWVNKTGR-DASVHTLLDALET[↑]GERIAKOKIEDHLLSSGKF
 DR4 406 DALYAMLK[↑]WVNKTGR-NASHTLLDALERMEERHAK[↑]EKI[↑]QDLLVD[↑]SGKF
 Apo3/DR3 374 DQYEMIKRW[↑]RQQQP---AGLGAVYAALERMGLDGCVEDLRS
 TNFR1 358 EAQYSMLATWRRRT[↑]ERREATLELLGRVLRDM[↑]DLG[↑]CLEDIEE
 CD95 256 EQKVQLLRNWHQLHGKKEAY-DT[↑]LIKDLK[↑]KANLCTLAERIQ[↑]T

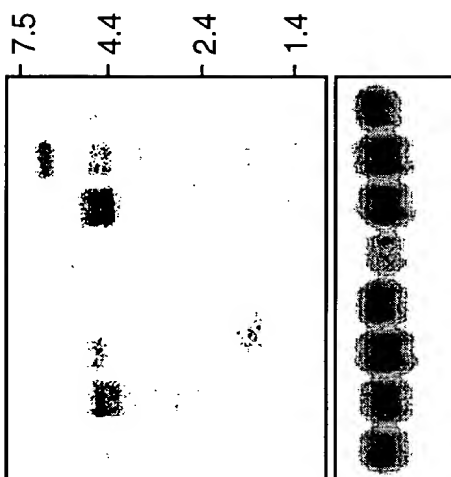
Apo2 400 MYLEGNADSALS
 DR4 455 IYLEDGTGSAVSLE

FIG._2

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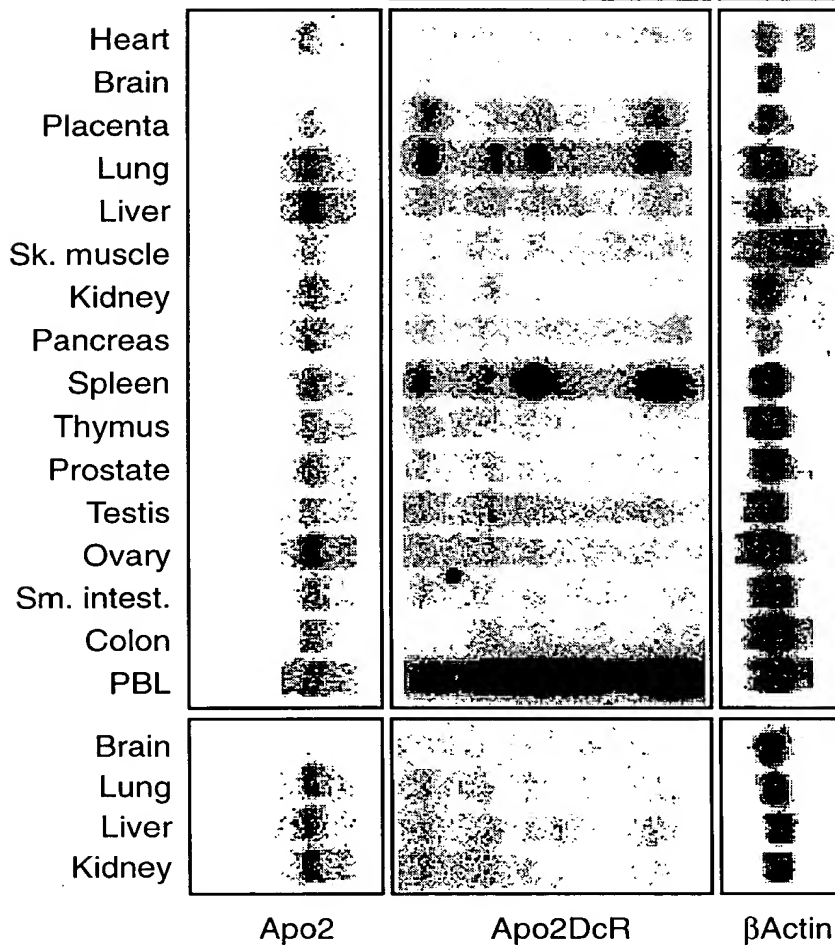
**FIG._3****FIG._4****FIG._5**

**FIG. 6****FIG. 10**



Cell Line

FIG. 7B



Adult

Fetal

FIG. 7A

1 CCCACGGCTC CGCATAAATC AGCACGGCGC CGGAGAACCC CGCAATCTCT GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAC
GGTGCCGAG CGGTATTAG TCGTGCGCGG GCCTCTTGG GCGGTAGAG GCGGGTGT TTATGTGGCT GCTACGGGCT AGATGAAATT CCGGACTTTC

101 CCACGGGGCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAAACAAC GGGACAGAAC GCGCGGGCGG CTTCGGGGGG CCGGAAAAGG CACGGGCCAG
GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTGTCTGC CCCTGTCTTG CCGGGCGGCG GAAGCGCGCG GGCCTTTTCC GTGCCGGGTC

1 M etGlucInAr gGlyGlnAsn AlaProAla laSerGlyAl aArgLysArg HisGlyProGly

201 GACCCAGGGA GCGCGGGGGA GCCAGGCCTG GGCTCCGGGT CCCAAGACC CTTGTGCTCG TTGTGCGCGG GGTCTGCTG TTGGTCTCAG CTCAGTCTGC
CTGGGTCCCT CCGCGCCCT CCGTCCGGAC CCGAGGCCCA GGGTTCTGG GAACACGAGC AACAGCGGCG CCAGGACGAC AACCAGAGTC GACTCAGACG

22 ProArgG1 uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSera laGluSerAla

301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCACAAAC AAAAGAGGTC CAGCCCCCTCA GAGGATTGT GTCCACCTGG ACACCATATC
AGACTAGTGG GTTCTTCTGG ATCGAGGGGT CGTCTCTCGC CGGGTCTTG TTTTCTCCAG GTCGGGGAGT CTCCTAACA CAGGTGGACC TGTGGTATAG

55 LeuIleThr GlnGlnAspL euAlaProG1 nGlnArgAla AlaProGlnG lNlysArgSe rSerProSer GluclyLeuC ysProProG1 yHisHisIle

401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT
AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CCGGACGTGG TCCACACTAA

88 serGluAspG lyArgaspCy sIleSerCys LysTyrGlyG lNAspTyrSe rThrHisTrip AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGGGAG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCCG
GTCCACTTCA CCTCGATTCA GGCACGTGGT GCTGGTCTTT GTGTACACA GTACAGCTTC TTCCGTGGAA GGCCTTCTT CTAAGAGGAC TCTACACGGC

122 GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luglyThrph eArgGluGlu AspSerProG luMetCysArg

601 GAAGTGCCG ACAGGGTGT CCAGAGGGAT GGTCAGGTC GGTCAAGGTC CACCTGGAG TGACATCGAA TGTGTCCACA AGAATCAGG CATCATCATA
CTTCACGGCG TGTCCACAG GGTCTCCCTA CCAGTTCCAG CCCTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT

155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyaspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerG1 yIleIleIle

701 GGAGTCACAG TTGAGCCGT AGTCTTGATT GTGGCTGTGT TTCTTTGCAA GTCTTTACTG TGAAGAAGG CCTGAAAGGC ATCTGCTCAG
CCTCAGTGC AACGTGGCA TCAGAACTAA CACCGACACA AACAAAGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC

188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly

801 GTGGTGGTGG GGACCCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCTCTCA AGATATCTTGC AGCCACCCCA
CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTCT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
222 GlyGlyG1 yAspProGlu ArgValAspA rgSerSerG1 nargProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG InProThrGln
901 GGTCCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
CCAGGGACTC GTCCCTTTACC TTCAGGTCCT CGGTCTCTC GGTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCCT
255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alAsnMetLe uSerProGly GluSerGluH isLeuLeuG1 uProAlaGlu
1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTGA TGACTTTGCA GACTTGGTGC
CGACTTTCCA GAGTCTCCTC CTCGACGAC CAAGGTCGTT TACTTCCACT AGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCCACG
288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG InCysPheAs pAspPheAla AspLeuValPro

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FIG.-8A-2

1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAGC TGAGGCAGCG GCCACAGGG ACACCTTGTA
 GGAAGCTGAG GACCCTCGG GAGTACTCCT TCAACCCGGA GTACTCTGTA CTCTATTTC ACCGATTTC ACTCGTCCG CCGGTGTCCC TGTGGAACAT
 322 PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr
 1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCCAGAT CCTCTGTCC ACACCTGCTT GGATGCCCTT GAGACCTGG GAGAGAGACT TGCCAAAGCAG
 GTGCTACGAC TATTTCACCC AGTTGTTTTT GCCCGCTTA CGGAGACAGG TGTGGGACGA CCTACGGAAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC
 355 ThrMetLeu ileLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln
 1301 AAGATTGAGG ACCACTTGTG GAGCTCTGGA AAGTTCAATG ATCTAGAAGG TAATGCACAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
 TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAAAC GGAATTCACAC TAAGAGAAGT CCTTCACTCT
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluG lYAsnAlaAsp SerAlaXqqs erOC*
 1401 CCTTCCCTGG TTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC
 GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGACTG GCCATGACCT TCTTTGAGAG
 1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCT TTCACTGCAC TTGCCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT
 GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTTC ACTTACACTA TTATTCTCTGT GATACCTTTA
 1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTTGGT TGGGATGTCA TTGTTTTTTC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
 CAGACCTAGT AAGGCAACA CCGATGAAC CCGATGAAC ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA
 1701 TTGGGCTACA TTGTAAGATC CATCTACAA AAAAAAAAAA AAAAAAAAAA GCGGCGCGG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
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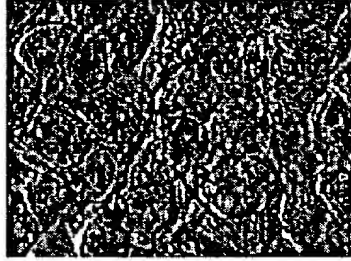
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FIG.-8B

1 MEQRGQNA PAASGARKRHGPGPREARGARPLRVPKTLVLVAAVLLVSAESALITQOD
 61 LAPQORAA PQQRSSPSEGLCPPGHHSIEDGRDCISCKYQDYSTHWNDDLFLCLRCTRCD
 121 SGEVELSPCTTTRNTVQCEEGTFREEDSPENCKRTGCPRGVMKVGDCTPWSDIQVH
 181 KESGIIIGVTAAVVLIVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDSSQRPGEAD
 241 NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRRLVPA
 301 NEGDPTETLRQCFFDADLVFPDSWEPLMRKLGMDNEIKVAKAEAGHRDLYTMLIKW
 361 VNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS

FIG.-9

Vector



Apo2



Apo2+CrmA

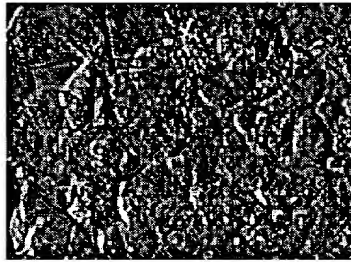
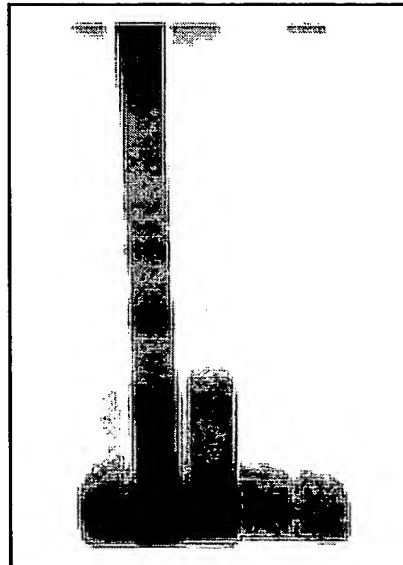


FIG._11A



Vector

Apo2

Apo2+CrmA

Apo2+DEVD

Apo2+ZVAD

FIG._11B

09887879.092001
T00260* 62828860

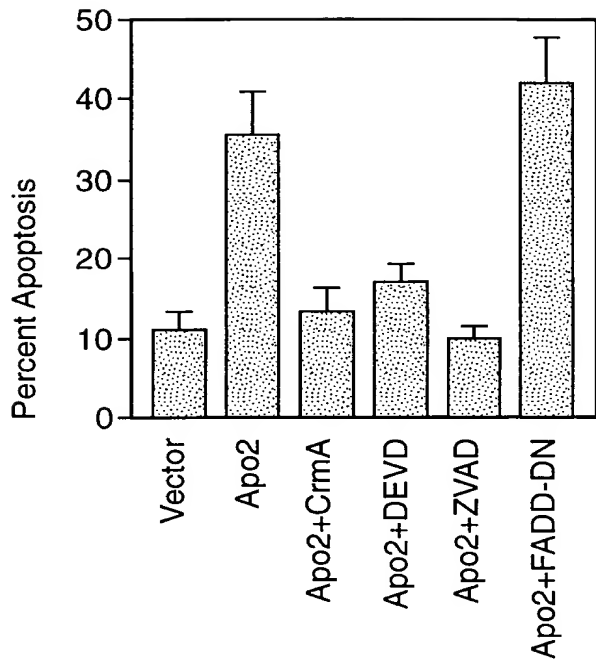


FIG. 11C

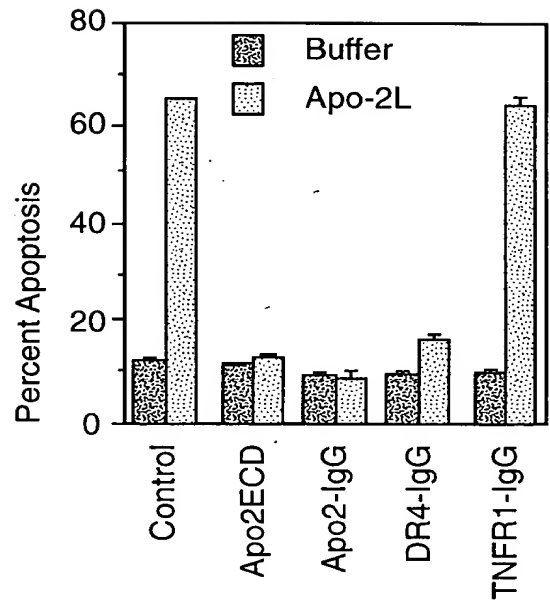


FIG. 11D

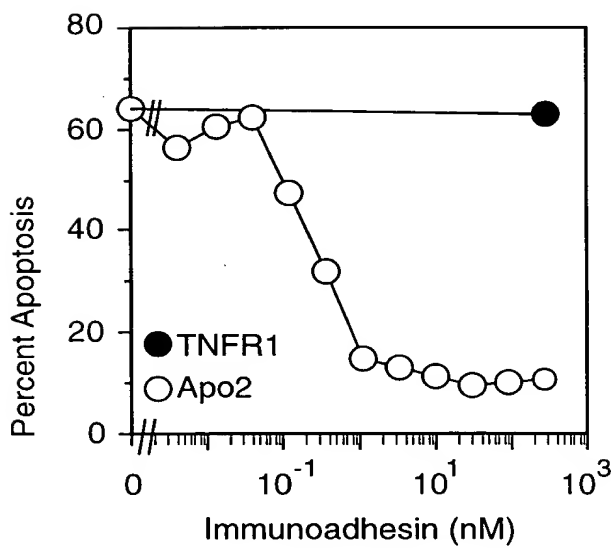


FIG. 11E

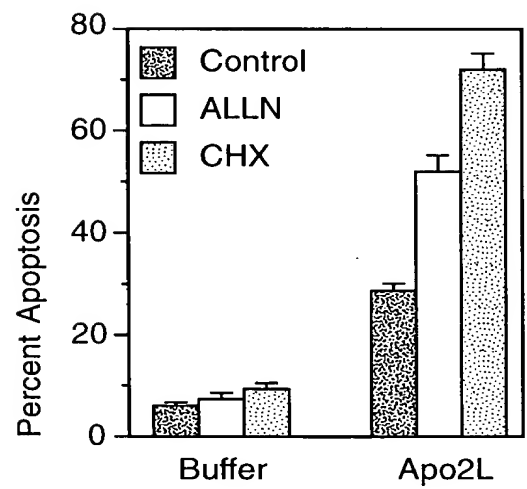
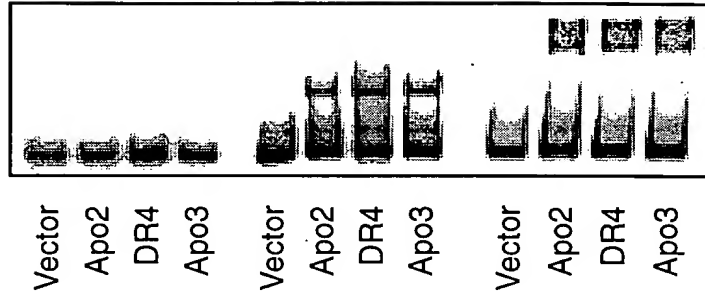
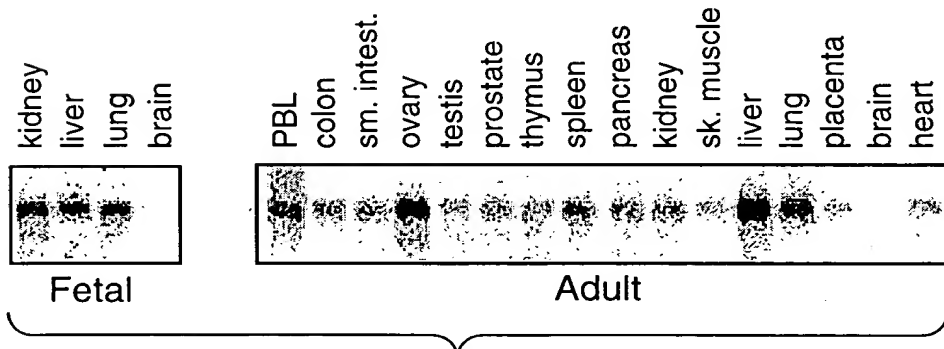
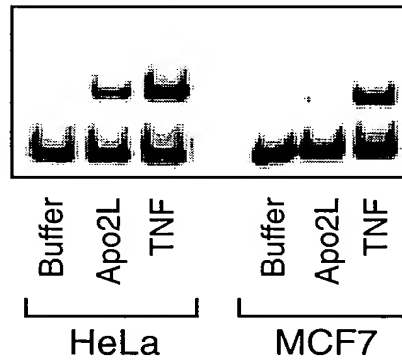


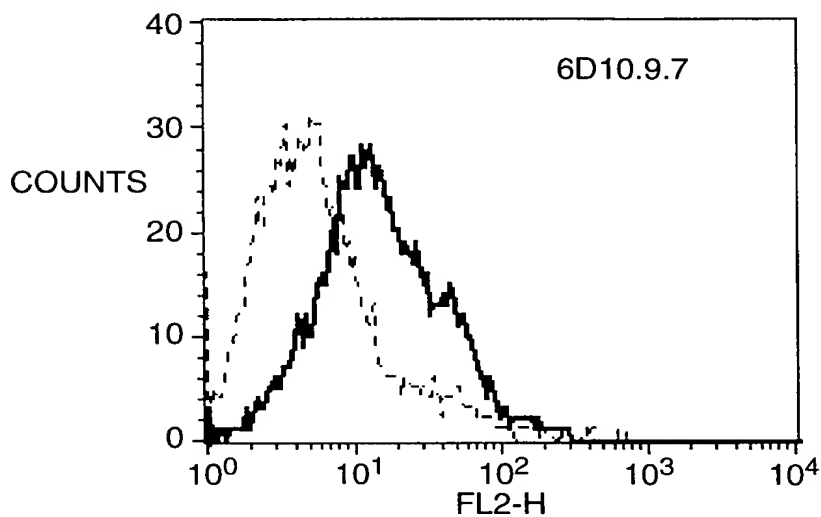
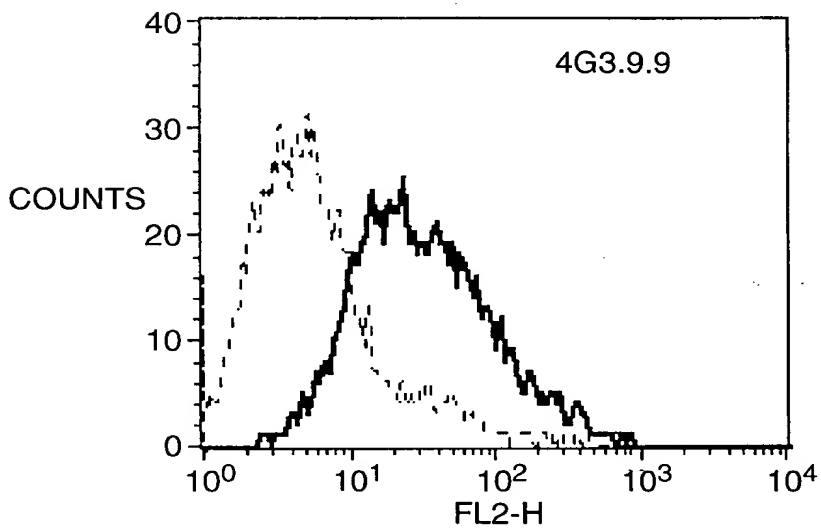
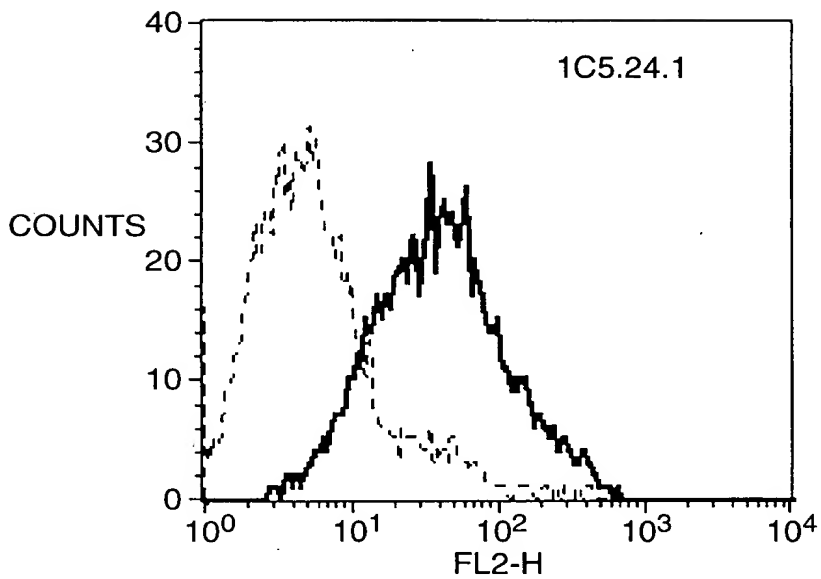
FIG. 12C

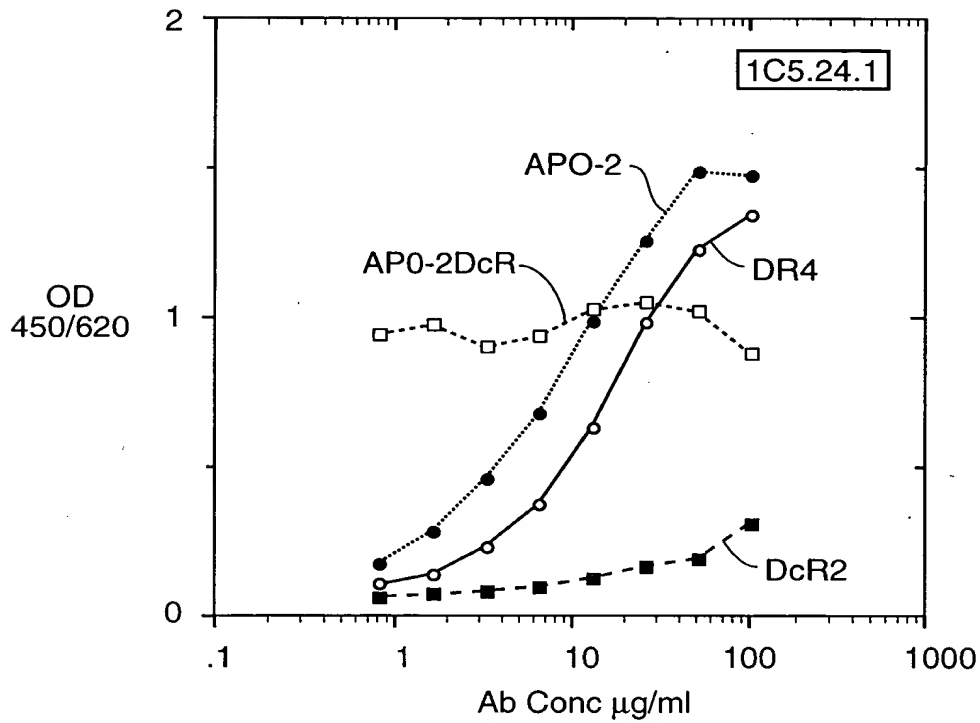
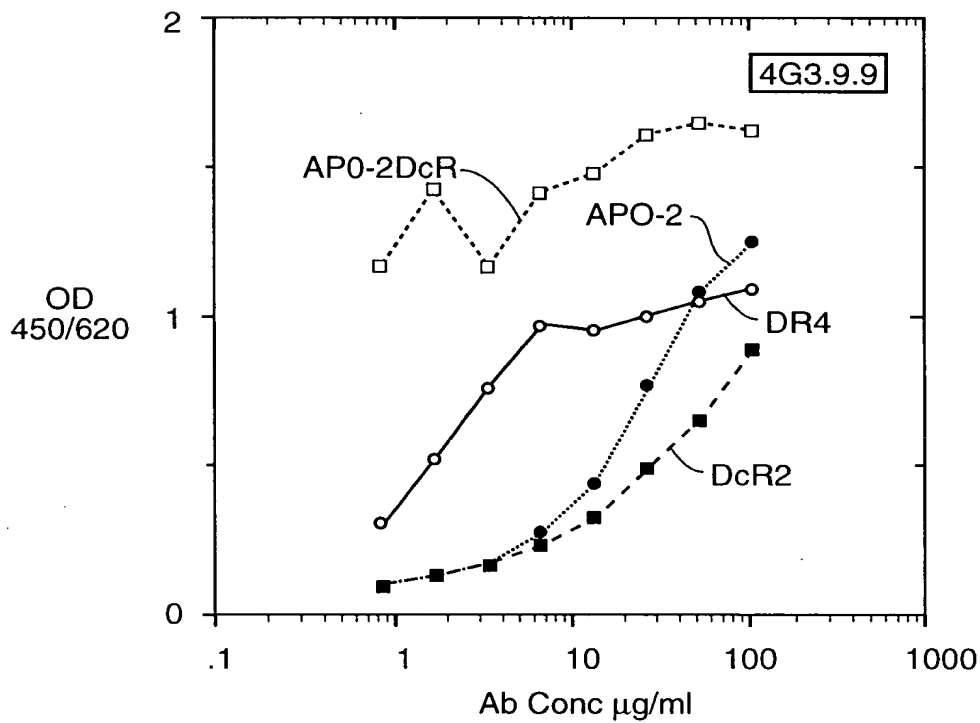
Unlabelled probe	+	+	+	+	-	-	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-	-	-	+	+	+	+

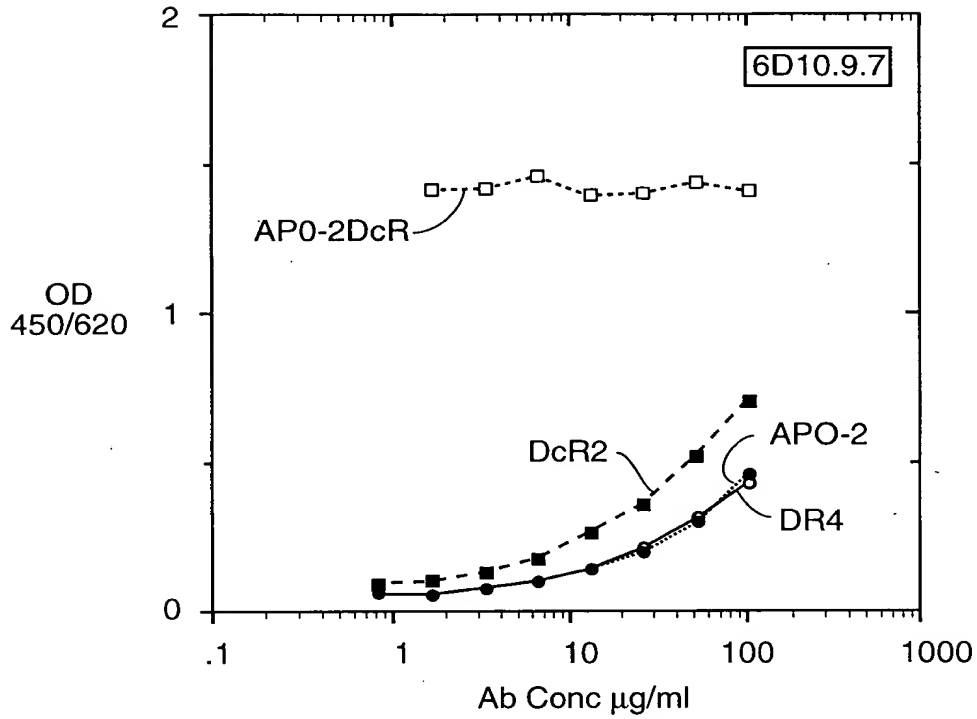
FIG. 12A

Unlabelled probe	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-

FIG. 12B**FIG. 13**



**FIG. 15A****FIG. 15B**

**FIG._15C**

Summary of mAbs to DcR1

mAbs	ISOTYPE	FACS (HUMEC)	DR4	Cross reactivity		
				Apo-2	Apo-2DcR	DcR2
1C5.24.1	IgG1	+	++	+++	+++	-
4G3.9.9	IgG1	+	++	+	+++	+/-
6D10.9.7	IgG2b	+	-	-	+++	+/-

Percent Cross reactivity was determined by comparing the binding capacity to Apo-2DcR at 10 µg/ml of mAbs in ELISA. ++: >75%, +: 25-75%, +/-: 10-25%, -: <10%.

FIG._16